FASTA searches a protein or DNA sequence data bank
version 3.3t05 March 30, 2000
Please cite:
W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

/tmp/fastaFAA4GaWRi: 704 aa
>SEQ ID NO:2
vs /tmp/fastaGAA5GaWRi library
searching /tmp/fastaGAA5GaWRi library

    704 residues in   1 sequences

FASTA (3.34 January 2000) function [optimized, BL50 matrix (15:-5)] ktup: 2
 join: 38, opt: 26, gap-pen: -12/ -2, width: 16
 Scan time: 0.033 .
The best scores are: opt
gi|12583612|emb|CAC27329.1| neurolysin [Homo sapi (704) 4666

>>gi|12583612|emb|CAC27329.1| neurolysin [Homo sapiens]
   (704 aa)
 initn: 4666 init1: 4666 opt: 4666
Smith-Waterman score: 4666; 100.000% identity in 704 aa overlap (1-704:1-704)

```
              10        20        30        40        50        60
SEQ    MIARCLLAVRSLRRVGGSRILLRMTLGREVMSPLQAMSSYTVAGRNVLRWDLSPEQIKTR
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|125 MIARCLLAVRSLRRVGGSRILLRMTLGREVMSPLQAMSSYTVAGRNVLRWDLSPEQIKTR
              10        20        30        40        50        60

              70        80        90       100       110       120
SEQ    TEELIVQTKQVYDAVGMLGIEEVTYENCLQALADVEVKYIVERTMLDFPQHVSSDKEVRA
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|125 TEELIVQTKQVYDAVGMLGIEEVTYENCLQALADVEVKYIVERTMLDFPQHVSSDKEVRA
              70        80        90       100       110       120

             130       140       150       160       170       180
SEQ    ASTEADKRLSRFDIEMSMRGDIFERIVHLQETCDLGKIKPEARRYLEKSIKMGKRNGLHL
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|125 ASTEADKRLSRFDIEMSMRGDIFERIVHLQETCDLGKIKPEARRYLEKSIKMGKRNGLHL
             130       140       150       160       170       180

             190       200       210       220       230       240
SEQ    PEQVQNEIKSMKKRMSELCIDFNKNLNEDDTFLVFSKAELGALPDDFIDSLEKTDDDKYK
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|125 PEQVQNEIKSMKKRMSELCIDFNKNLNEDDTFLVFSKAELGALPDDFIDSLEKTDDDKYK
             190       200       210       220       230       240

             250       260       270       280       290       300
SEQ    ITLKYPHYFPVMKKCCIPETRRRMEMAFNTRCKEENTIILQQLLPLRTKVAKLLGYSTHA
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|125 ITLKYPHYFPVMKKCCIPETRRRMEMAFNTRCKEENTIILQQLLPLRTKVAKLLGYSTHA
             250       260       270       280       290       300

             310       320       330       340       350       360
SEQ    DFVLEMNTAKSTSRVTAFLDDLSQKLKPLGEAEREFILNLKKKECKDRGFEYDGKINAWD
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|125 DFVLEMNTAKSTSRVTAFLDDLSQKLKPLGEAEREFILNLKKKECKDRGFEYDGKINAWD
             310       320       330       340       350       360

             370       380       390       400       410       420
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SEQ      LYYYMTQTEELKYSIDQEFLKEYFPIEVVTEGLLNTYQELLGLSFEQMTDAHVWNKSVTL
         :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|125   LYYYMTQTEELKYSIDQEFLKEYFPIEVVTEGLLNTYQELLGLSFEQMTDAHVWNKSVTL
             370       380       390       400       410       420


             430       440       450       460       470       480
SEQ      YTVKDKATGEVLGQFYLDLYPREGKYNHAACFGLQPGCLLPDGSRMMAVAALVVNFSQPV
         :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|125   YTVKDKATGEVLGQFYLDLYPREGKYNHAACFGLQPGCLLPDGSRMMAVAALVVNFSQPV
             430       440       450       460       470       480


             490       500       510       520       530       540
SEQ      AGRPSLLRHDEVRTYFHEFGHVMHQICAQTDFARFSGTNVETDFVEVPSQMLENWVWDVD
         :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|125   AGRPSLLRHDEVRTYFHEFGHVMHQICAQTDFARFSGTNVETDFVEVPSQMLENWVWDVD
             490       500       510       520       530       540


             550       560       570       580       590       600
SEQ      SLRRLSKHYKDGSPIADDLLEKLVASRLVNTGLLTLRQIVLSKVDQSLHTNTSLDAASEY
         :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|125   SLRRLSKHYKDGSPIADDLLEKLVASRLVNTGLLTLRQIVLSKVDQSLHTNTSLDAASEY
             550       560       570       580       590       600


             610       620       630       640       650       660
SEQ      AKYCSEILGVAATPGTNMPATFGHLAGGYDGQYYGYLWSEVFSMDMFYSCFKKEGIMNPE
         :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|125   AKYCSEILGVAATPGTNMPATFGHLAGGYDGQYYGYLWSEVFSMDMFYSCFKKEGIMNPE
             610       620       630       640       650       660


             670       680       690       700
SEQ      VGMKYRNLILKPGGSLDGMDMLHNFLKREPNQKAFLMSRGLHAP
         ::::::::::::::::::::::::::::::::::::::::::::
 |125    VGMKYRNLILKPGGSLDGMDMLHNFLKREPNQKAFLMSRGLHAP
             670       680       690       700



704 residues in 1 query    sequences
704 residues in 1 library sequences
 Scomplib [version 3.3t05 March 30, 2000]
 start: Fri Nov  1 15:59:40 2002 done: Fri Nov  1 15:59:41 2002
 Scan time:  0.033 Display time:  0.700

Function used was FASTA
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